

Wed May 7 14:14:34 2003

us-10-027-000-1.rst

Page 1

GenCore version 5.1.4-p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 3, 2003, 23:25:47 ; Search time 2710.34 Seconds
(without alignments)
17782.898 Million cell updates/sec

Title: us-10-027-000-1
Perfect score: 2976
Sequence: 1 ttatagtcgcttgcgttaaat.....aaaaaaaaaaaaaaaaaa 2976

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_estlum:*
3: em_estlin:*
4: em_estmu:*
5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estlom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	290.8	9.8	1056	17	CNS078CQ
2	254.6	8.6	503	17	AQ399568
3	227	7.6	1021	17	AQ399568
4	187.4	6.3	994	17	CNS0772N
5	184.6	6.2	970	17	CNS0755SU
6	176.8	5.9	1045	17	CNS07387

C	7	175.4	5.9	952	17	CNS0730C	AL427978	clone BAO
C	8	171.8	5.8	812	17	CNS072MT	AL426403	clone BAO
C	9	167.2	5.6	917	17	CNS070R	AL423994	T3 end of
C	10	165.4	5.6	745	17	CNS072H1	AL426203	clone BAO
C	11	158.6	5.3	993	17	CNS078JU	AL434074	T3 end of
C	12	158.4	5.3	986	17	CNS076GU	AL431380	T3 end of
C	13	153.4	5.2	836	17	CNS074WR	AL429361	clone BAO
C	14	126.2	4.2	860	17	CNS077OT	AL430279	T3 end of
C	15	120.6	4.1	869	17	CNS075M9	AL431963	T7 end of
C	16	115.6	3.9	1010	17	CNS076X1	AL714457	clone BAO
C	17	115.4	3.9	633	9	AL714457	AL714436	AL714436
C	18	115.4	3.9	684	9	AL714436	AL714436	AL714436
C	19	115	3.9	521	17	AZ928908	AL228808	479. dif19
C	20	109.2	3.7	984	17	CNS070OH	AL423879	T3 end of
C	21	104.6	3.5	573	12	BE805639	BE805639	ss43f04.y
C	22	82.4	2.8	1000	17	CNS072XT	AL426807	clone BAO
C	23	82.2	2.8	1132	13	BM320864	BM320864	rockefell
C	24	79.8	2.7	865	17	CNS07709	AL433015	T3 end of
C	25	79.2	2.7	376	9	AL513757	AL513757	AL513757
C	26	76.8	2.6	610	9	AL827475	AL827475	AL827475
C	27	75.4	2.5	781	17	CNS0726L	AL425827	clone BAO
C	28	75.4	2.5	1012	17	CNS0772L	AL433351	T3 end of
C	29	72.6	2.4	861	10	BE636906	BE636906	rockefell
C	30	72.2	2.4	331	10	BE059900	BE059900	sn38f02.y
C	31	71.8	2.4	194	10	AW184930	AW184930	se83q11.y
C	32	71.6	2.4	997	14	BQ276931	BQ276931	AGENCOURT
C	33	71.6	2.4	1165	13	BM320900	BM320900	rockefell
C	34	71.6	2.4	1057	13	BM321375	BM321375	rockefell
C	35	70.8	2.4	226	12	BG792492	BG792492	UTSW_H38A
C	36	70.8	2.4	226	12	BG817252	BG817252	UTSW_H20A
C	37	70.8	2.4	486	9	AW346777	AW346777	29458 MAR
C	38	70.4	2.4	231	10	BM782468	BM782468	KH26B06.y
C	39	70.4	2.4	266	13	B1782468	B1782468	mcct001xa
C	40	70.4	2.4	641	12	BE0809574	BE0809574	BE040678
C	41	70.4	2.4	824	10	BE040678	BE040678	L336c.d
C	42	70.2	2.4	705	17	BH019836	BH019836	L14841.d
C	43	70.2	2.4	732	17	BH018404	BH018404	rockefell
C	44	70.2	2.4	853	13	BM321393	BM321393	rockefell
C	45	70	2.4	358	9	AL515173	AL515173	AL515173

ALIGNMENTS

RESULT 1
CNS078CQ/c
LOCUS
DEFINITION
T3 end of clone BB0AA019F09 of library BB0AA from strain CBS 4732

ACCESSION
AL433824
VERSION
AT433824.1 GI:12217238

KEYWORDS
SOURCE
ORGANISM
GSS.
Pichia angusta.
Pichia angusta
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.

REFERENCE
AUTHORS
Souclet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
de-Montigny,J., Dujon,B., Durieux,P., Lepointe,A., Lorente,B.,
Malpertuy,A., Neuvéglise,C., Ozier-Kalogiropoulos,O., Potier,S.,
Saurin,W., Tekata,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.

TITLE
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies

JOURNAL
MEDLINE
PUBMED
20584711
11152876

REFERENCE
AUTHORS
TITLE
2 (bases 1 to 1056)
Blandin,G., Lorente,B., Malpertuy,A., Wincker,P., Artiguenave,F.,
and Dujon,B.
Genomic exploration of the hemiascomycetous yeasts: 13. Pichia
angusta

/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25x genome coverage. High density colony filters
are available upon request."

BASE COUNT 101 a 168 c 146 g 88 t
ORIGIN

Query Match 8.6%; Score 254.6; DB 17; Length 503;
Best Local Similarity 74.6%; Pred. No. 6.7e-25;
Matches 320; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 408 GGTATCGACTCTGGACACAAAGGCTCTCCCAAGCATGAGATCCCTCTCCGCTT 467
DB 75 GGTATCGACTCTGGACACAAAGGCTCTCCCAAGCATGAGATCCCTCTCCGCTT 467
QY 468 ACAGATGAGCCCAACGAGCGCTAAGAGGACCAAGTTTCAATGGCCCTCTGGGCTGC 527
DB 135 TCAGACGGCCCAACGAGCGCTAAGAGGACCAAGTTTCAATGGCCCTCTGGGCTGC 527
QY 528 TTCCCTGGGCGGACGCTGCTGCTCCATTCACCAAACTCTCTCGAAGGACGAT 587
DB 195 TTCCCTGGGCGGACGCTGCTGCTCCATTCACCAAACTCTCTCGAAGGACGAT 587
QY 588 AAGATGATGGGCAAGAGGCGCTCTAAGAGTGGATGATCTCTGGGCTGC 647
DB 255 CGAAGATGATGGGCAAGAGGCGCTCTAAGAGTGGATGATCTCTGGGCTGC 647
QY 648 AACATCGACGCTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 707
DB 315 AACATCGACGCTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 707
QY 708 CTGGCGGCTTGGAGCTGCGGCTCTCATCCGCGCATTCAGAGCATGAGTGCAGCT 767
DB 375 CTGGCGGCTTGGAGCTGCGGCTCTCATCCGCGCATTCAGAGCATGAGTGCAGCT 767
QY 768 ACATCAAGACCTTTTGTGCAATATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAG 827
DB 435 ACATCAAGACCTTTTGTGCAATATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAG 827
QY 828 GTCCAGGAG 836
DB 495 CTGACGCGG 503

RESULT 3
CNS0766A 1021 bp DNA linear GSS 07-JUL-2001
LOCUS 17 end of clone BB0A001C03 of library BB0A from strain CBS 4732
DEFINITION of *Pichia angusta*, genomic survey sequence.

ACCESSION AL431000
VERSION AL431000.1 GI:12214412
KEYWORDS GSS.
SOURCE *Pichia angusta*.
ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; *Pichia*.

REFERENCE 1 (bases 1 to 1021)
Souchet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Boulet, J., Bon, E., Brothier, P., Casaregola, S.,
de Montigny, J., Dujon, B., Durieux, P., Lepoint, A., Llorente, B.,
Malpertuy, A., Neugebauer, C., Ozier-Lalonde, O., Pollet, S.,
Saurin, W., Tekala, F., Toffanin-Moche, C., Wesolowski-Louvel, M.,
Wincker, P., and Weissenbach, J.

Genomic exploration of the hemiascomycetous yeasts: 1. A set of

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
angusta
FERS Lett. 487 (1), 76-81 (2000)
20584723
11152876
2 (bases 1 to 1021)
Blandin, G., Llorente, B., Malpertuy, A., Wincker, P., Artiguenave, F.,
and Dujon, B.
Genomic exploration of the hemiascomycetous yeasts: 13. *Pichia*

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
angusta
FERS Lett. 487 (1), 76-81 (2000)
20584723
11152888
3 (bases 1 to 1021)
Genoscope.
Direct Submission
Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage,
2 rue Gaston Cremlieux, CP 5706, 91057 Evry cedex, FRANCE. (E-mail :
sequel@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: *Saccharomyces bayanus* var. *uvarum*, *Saccharomyces*
exiguus, *Saccharomyces servazii*, *Zygosaccharomyces rouxii*,
Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces*
lactis var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia sorbitophila*,
angusta, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*,
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.

COMMENT

FEATURES
source
1..1021
/organism="Pichia angusta"
/strain="CBS 4732"
/db_xref="taxon:4905"
/clone="BB0A001C03"
/clone_11b="BB0AA"
/note="end : T7"
misc-feature
/note="similar to P07337 [Beta-glucosidase precursor BGIS
] [Kluyveromyces marxianus]"
/evidence="not_experimental"

BASE COUNT 260 a 231 c 278 g 247 t 5 others
ORIGIN
Query Match 7.6%; Score 227; DB 17; Length 1021;
Best Local Similarity 54.6%; Pred. No. 2.3e-21;
Matches 513; Conservative 3; Mismatches 414; Indels 9; Gaps 3;

QY 1745 GTACGTAGACGACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1804
DB 3 GTTGTGGAGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 62
QY 1805 CTTCGGCTCCGACACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1864
DB 63 CTATGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 122
QY 1865 CAAGTTCAAGATGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1921
DB 123 VTGTTTCGATGATGAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 182
QY 1922 GTTCCCGGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1981
DB 183 CTGTTTGGAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 242
QY 1982 AATCGAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2041
DB 243 GATTCAGACGAGCAGAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 302
QY 2042 TTAACGCGACTGGAGACGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTGCT 2101
DB 303 CAATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 362
QY 2102 GGACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2161

Db 363 CGACGCCCTAATAGACTCGTCTTGAGACCAATCCGTGACAGTCTGTGATTACAGGC 422

QY 2162 GGGACACCCCGGAGAGATGCTGCTGACGACCCAGCCCGCTCAATCCAGGCTGTA 2221

Db 423 AGGAGCGCAGTGAATAGCTTGGAGAGACCAAGCAAGCTTACTGACACTCTTGA 482

QY 2222 GGGCGGCAACGAGACGAGCACTCCATTGCGGACGTCTCTTTGGACATACACCCCTC 2281

Db 483 GGGCGGCAACGAGACGAGCACTCCATTGCGGACGTCTCTTTGGACATACACCCCTC 542

QY 2282 GGGGAGCTGTGCTCAGCTTCCCAAGCCGCTGACAGACACCCCGCTTCTCAACTT 2341

Db 543 TGGGAGCTGTGCTCAGCTTCCCAAGCCGCTGACAGACACCCCGCTTCTCAACTT 602

QY 2342 CCGGACCCAGCGCGGCGGCGACGCTGTACGGGAGAGCTGTGCGGTACAGTACTA 2401

Db 603 CGGACCAAGAAAAGCGAGGGGTTCTGTATGAGATGTTAGTTGGCTACCGCTTTTA 662

QY 2402 CGAGTTTCCGACAGACGCTCAATTTCCCTTTGGCCAGCGCTGCTTCAACACTTT 2461

Db 663 CGATCACTGGGTGTCTGTACGCTGTTTCAATTCGGCCAGCGGCTGACGCTACTTT 722

QY 2462 TGCCTTTTCAATCTCTCCGTCTGCTCACAAGACGAGCACTGAGCGTGTCCCTCCGT 2521

Db 723 TGTCTGTCTGATTAAAGTG---CACTACGACGACATCTCTGAGCTTGAAGTTTGGC 779

QY 2522 GAAAGAACCGGCTCCGCTGCGCGGCGACAGTGTGCGCCAGCTCTACGTAAGCCCTCCA 2581

Db 780 GAAAGAACCGGCTCCGCTGCGCGGCGACAGTGTGCGCCAGCTCTACGTAAGCCCTCCA 839

QY 2582 AGCGCCAGATTAACCGCCCGCTCAAGAGCTCAAGGGCTTCCGCAAGCTGGAAGTGA 2641

Db 840 CCCAGC---AATTAAGGGGCGCATTCAAAGAGCTGAAAGATTTAGCAAGATATTCTGGA 896

QY 2642 GCGCGGGAACGAGAGCGGCTGACATTCGAGAGCAGGA 2680

Db 897 RCAGGAAGCTCAGAAATTTGTATTCATCATCAACGGA 935

RESULT 4
CONS0772N/c 994 bp DNA linear GSS 08-JUL-2001
LOCUS T3 end of clone BBOAA015H01 of library BBOAA from strain CBS 4732
DEFINITION of *Pichia angusta*, genomic survey sequence.
ACCESSION AL433353
VERSION AL433353.1 GI:12216767
KEYWORDS GSS.
SOURCE *Pichia angusta*.
ORGANISM *Pichia angusta*.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
REFERENCE 1 (bases 1 to 994)
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bollotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
de-Montigny,D., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neugeglise,C., Ozler-Kalogeropoulos,O., Potter,S.,
Sautin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
PUBMED 11152876
REFERENCE 2 (bases 1 to 994)
AUTHORS Blandin,G., Llorente,B., Malpertuy,A., Wincker,P., Artiguenave,F.
and Dujon,B.
TITLE Genomic exploration of the hemiascomycetous yeasts: 13. *Pichia*
angusta
JOURNAL FEBS Lett. 487 (1), 76-81 (2000)
MEDLINE 20584723
PUBMED 11152888
REFERENCE 3 (bases 1 to 994)
AUTHORS Genoscope.

TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This GSS is part of a random genomic sequencing program of thirteen
yeast species: *Saccharomyces bayanus* var. *uvarum*, *Saccharomyces*
exiguus, *Saccharomyces servazii*, *Zygosaccharomyces rouxii*,
Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces*
lactis var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia*
angusta, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*,
Candida tropicalis and *Yarrowia lipolytica*. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
FEATURES
Source
Location/Qualifiers
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/organism="Pichia angusta"
/strain="CBS 4732"
/db_xref="taxon:4905"
/clone="BBOAA015H01"
/clone_11b="BBOAA"
/note="end : T3"
complement(<24..>992)
/note="similar to P07337 [Beta-glucosidase precursor BGIS
] [Kluyveromyces marxianus]"
/evidence="not experimental"
BASE COUNT 291 a 235 c 192 g 276 t
ORIGIN
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Best Local Similarity 51.2%; Pred. No. 4.4e-16;
Matches 490; Conservative 0; Mismatches 461; Indels 6; Gaps 2;
QY 960 CTGATGSGATGCTGTAAGAAAGATGGGTGGATGCTTATATAGAGCACTGTAC 1019
Db 977 CTCACGTGTGTCTGTGAGAGATGGGTGGATGCTTATATATGCTGAGTGT 918
QY 1020 GGCACATACAGTACACACAGAGCCGTTGGGCGCCTCGACATGCCGAGACT 1079
Db 917 GGTGTCTACTCGATCAAAAATTTCTATTTGAGAGTTTGAGCTGAGTGTCCGAGCTT 858
QY 1080 CCACGCTCCGAGAGAAACACTCAAGTTCAACGTTCCAA---CGAAACCCCTTATC 1136
Db 857 CCATCATAGAAAATAATGATGACGTGTACACGCTATCAATGACAGAGATCAGATA 798
QY 1137 CAGCTATTGACAGAGGCGCTAGGAGATGCTTTCGCTGTCAGAAAGTGTGCTCC 1196
Db 797 GACGTATTGATGAAGAAGATTGAAAGCTGCTGAACTGTGGAGATTTTCTATGCAAGC 738
QY 1197 GGAATGACGAGAGAGCGCCCGGAGACGCTGCAACACACCCGAAACGAGACTCTC 1256
Db 737 GGCATTCTGAAAATATGCTCTGAAATATCTTAAGATATATGCTGAGACTCTGCTTG 678
QY 1257 CTCGGAAGGTTGGCAACAGAGGCGATGCTGCTGTGAAGAAGCAACAGTTTGC 1316
Db 677 CTCAAAAGGCTAGCTCGAAGATCTCTGTGCTGGAAGATTAAGATTTTGGCT 618
QY 1317 TTGACCAAGAAAGAAAGACCTGATTTGTGCGCCCAAGCGCAAGAGCGACATACAC 1376
Db 617 TTGAAAAGAGGAAATATATGCTGTGATTTGGCTTAAACCTTAAGTTCTTAATATCTT 558
QY 1377 GCGGAGGCTTGCCCGACACTGAGGCGCTTACAGCACTGCTCCCTTTGAGCGCTCAGC 1436
Db 557 GGTGGGGCTCTGCTGATGATATCTTATATGCTCAAAATTTTGTATGATTTGCT 498
QY 1437 AAGCAGCTCGAGAGCGGCACTGATACCGTGGCGGCTACACACCGTCTCCATT 1496
Db 497 GATTAATTTAGAGAGCCCACTATGCTGATGATGTTGCTCAATTAAGAAAACCTGCTC 438
QY 1497 CTAGCGAGAGTCTTCACGCGGCGAGCGGCTCGGAGATGGCTGAGAGGCTCTCAAC 1556
Db 437 GATCTGGGACCTTGTCTACCTTCAACGCTTCGAAAGGGTTATTGCAAGGTTTACAGC 378

Db 191 ATTGTCACCAAGCCAAAGAGGCTTCTTCTGAGGTGGTCTGATCATATGACCT 132
 QY 1404 TACTACAGCAGTCTCCCTTTGACGGCTCAGCAGAGCAGTCCAGAGCCCGCATCTGAC 1463
 Db 131 TACTATGTTATTTCACTTACAGAGGATCGTCAGAAAGTGGCAGAGGATACCATAT 72
 QY 1464 ACCGTCGGCGC 1474
 Db 71 ACAATTGGGGC 61

RESULT 6

CNS07387/c

LOCUS 1045 bp DNA linear GSS 07-JUL-2001
 DEFINITION clone BA0AB017E12 of library BA0AB from strain CLIB 210 of
 Kluyveromyces lactis, genomic survey sequence.

ACCESSION

AL427181

VERSION

AL427181.1 GI:12210375

KEYWORDS

GSS.

SOURCE

Kluyveromyces lactis.

REFERENCE

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Kluyveromyces.

AUTHORS

1 (bases 1 to 1045)
 Souciet,J.L., Algie,M., Artiguenave,F., Blandin,G.,
 Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
 de-Montigny,J., Dujon,B., Durans,P., Lepingle,A., Liorette,B.,
 Malpertuy,A., Neugeglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
 Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
 Wincker,P. and Weissenbach,J.

TITLE

Genomic exploration of the hemiascomycetous yeasts: 1. A set of
 yeast species for molecular evolution studies

JOURNAL

FEBS Lett. 487 (1), 3-12 (2000)

MEDLINE

20584711

PUBMED

11152876

REFERENCE

2 (bases 1 to 1045)
 Bolotin-Fukuhara,M., Toffano-Nioche,C., Artiguenave,F.,
 Duchateau-Nguyen,G., Lemaire,M., Marmelisse,R., Montrocher,R.,
 Robert,C., Termier,M., Wincker,P. and Wesolowski-Louvel,M.

AUTHORS

Genomic exploration of the hemiascomycetous yeasts: 11.
 Kluyveromyces lactis

TITLE

Genomic exploration of the hemiascomycetous yeasts: 11.
 Kluyveromyces lactis

JOURNAL

FEBS Lett. 487 (1), 66-70 (2000)

MEDLINE

20584721

PUBMED

11152886

REFERENCE

3 (bases 1 to 1045)
 Genoscope.

AUTHORS

Direct Submission
 Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
 seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)

TITLE

This GSS is part of a random genomic sequencing program of thirteen
 yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
 exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii,
 Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
 lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
 angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
 Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
 5 kb were prepared and both extremities were sequenced. See
 keywords for description of this sequence and for the sequence of
 the other extremity of this insert.

COMMENT

Location/Qualifiers
 1. 1045

FEATURES

Location/Qualifiers
 1. 1045

SOURCE

1. 1045
 /organism="Kluyveromyces lactis"
 /strain="CLIB 210"
 /variety="lactis"
 /db_xref="taxon:28985"
 /clone="BA0AB017E12"
 /clone_1lb="BA0AB"

BASE COUNT

314 a 243 c 182 g 300 t 6 others

ORIGIN

Query Match 5.9%; Score 176.8; DB 17; Length 1045;
 Best Local Similarity 51.2%; Pred. No. 1.1e-14;

Matches 410; Conservative 1; Mismatches 390; Indels 0; Gaps 0;

QY 1959 AAGGTCAATTGAGACAGACAGCCGAAATGCAAAAGTCCGCGCCCGCAGAGACAGAC 2018
 Db 945 AAGGCTATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 886
 QY 2019 CAGGTTCATCATCTGCGCGGCTTACGCCGACATGAGAGACCGAGCGCCGACCGCG 2078
 Db 885 AAGGCTATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 826
 QY 2079 AGCATGAAGCTCCCGCGGCTGACAGCAGTCTTCCACATGAGCGCCGCAACCA 2138
 Db 825 GATATGACTTTGCGCAGAGAAAGCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 766
 QY 2139 AACACCGTCGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2198
 Db 765 AACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 706
 QY 2199 CCGGCGGTCATGACAGCGCTGTGATGAGCGGCAACGAGACGGAATGCTGCGACGTC 2258
 Db 705 AAMHHTCTCATTCAGGCTGTGACGAGGTAATGAGTGGCAATGCTATTGCTGATGTC 646
 QY 2259 GTCTTGGCGACTACCAACCCCTGGGCAAGCTGCTCCCTGAGTCCCAAGCGCTGCG 2318
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 QY 2319 GACACACCCCGCTTCTCAACTTCCGACCGAGCGCGGCGACGCTGACGAGGAGC 2378
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 Db 285 GATTCAGAAATTTTCTTCAACTGCGGCAAAACGAAACAGTCAAAAGTTGATTAATC 226
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RESULT 7

CNS0730C/c

LOCUS 952 bp DNA linear GSS 07-JUL-2001
 DEFINITION clone BA0AB023A01 of library BA0AB from strain CLIB 210 of
 Kluyveromyces lactis, genomic survey sequence.

ACCESSION

AL427978

VERSION

AL427978.1 GI:12211172

KEYWORDS

GSS.

SOURCE

Kluyveromyces lactis.

REFERENCE

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 1 (bases 1 to 952)
 Souciet,J.L., Algie,M., Artiguenave,F., Blandin,G.,

yeast species: *Saccharomyces bayanus* var. *uvatum*, *Saccharomyces exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES
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/evidence=not_experimental

BASE COUNT 246 a 193 c 159 g 261 t 1 others

ORIGIN

Query Match 4.28; Score 126.2; DB 17; Length 860;
Best Local Similarity 49.58; Pred. No. 6.5e-08;
Matches 357; Conservative 0; Mismatches 358; Indels 6; Gaps 1;

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1788 GTCCCGCGCGATGCTTCTGCGCTCCGCCACCGCGAGAGAGGCGCGCATCATCTC 1847
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1848 GTCAAGGCGCAACAGCTACAGTTCAAGATGAGTTGGGCTCCGACCCACCTACACCTC 1907
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1908 AAGGCGACACCATCTGCTCC-----CGGCCACGCGCTCCCTCCGCGCGGCGTGCAG 1961
482 GAGACCTTGTGATCTGTGGGATCAACGCGGAGGTTGTTGACTGTTGCAATTGGAGAA 423
1962 GTCATTTGACGACGCGGCGAATCGAATGCGCTCGCCCTCGCCAGAGACGACGACCA 2021
422 AAGATCCCTGATGAGTTCAGATTAAATGAGATGAGATGAGCAAAAAGAGTCGATAG 363
2022 GTCATCATCTGCGGCGCTTACGCGACATGAGAGACGAGGCGCGCGCGCGCGAGC 2081
362 GTCATCATCTTGTATTTGAAACCTCCCAACGATTTGAGAGCGAGGATTTGACCGGCTC 303
2082 ATGAAGCTCCCGCGGCGTGTGACGACGCTCATTTGCCGAGTGGCGCGCGCAACCAAC 2141
302 ATGAGATCTTCCAAACTTCAAAATTAAGCTTGTGACGAAATATCTGAATGAACGAGAC 243
2142 ACCGTCGTCGATGACGAGAGGCGACCCCGAGAGATGCGCTGCGACGCGCC 2201
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2202 GCGGTCATCCAGGCGCTGATGAGCGCGCAAGAGAGGCGCAATCATTCGACAGCTGTC 2261
182 GCACCTTTTACAGGAGATGTTTAATGGGATGATGATGAGAAATGCTAATTCAGACCTACTA 123
2262 TTGGGACTACAAACCCCTCGGCGAAGCTGCTCAGCTTCCCAAGGCGCTCGAGAGAC 2321
122 TTAGGAGAGGCTAATCTCTCGGAAAGCTTCTCTTTTGGCCTAGAGCTGTGAGAGAC 63
2322 AACCCGCGCTTCTCACTTCGCGACGAGGCGCGGCGGCGACGCTGTAGGCGCAGACGTC 2381

Db 62 AATCCTCTCTTTTAACTTAATCTGACATGCTAAGTTGCTATGCGGAGACGCT 3
Oy 2382 T 2382
Db 2 T 2

RESULT 15

CNS075W9

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 869)
Soullet, J. L., Aigle, M., Artiguenave, F., Blandin, G.,
Biolotin-Fukuhara, M., Bon, E., Brothier, P., Casaregola, S.,
de Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Lorente, B.,
Malpertuy, A., Neveglisse, C., Ozler-Kalogeropoulos, O., Potier, S.,
Saulin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissensbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

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JOURNAL

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REFERENCE

AUTHORS

TITLE

CNS075W9 869 bp DNA linear GSS 07-JUL-2001
clone BA0AB036G05 of library BA0AB from strain CLIB 210 of
Kluyveromyces lactis, genomic survey sequence.
AL30279.1 GI:12213473
GSS.
Kluyveromyces lactis.
Kluyveromyces lactis.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
1 (bases 1 to 869)
Soullet, J. L., Aigle, M., Artiguenave, F., Blandin, G.,
Biolotin-Fukuhara, M., Bon, E., Brothier, P., Casaregola, S.,
de Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Lorente, B.,
Malpertuy, A., Neveglisse, C., Ozler-Kalogeropoulos, O., Potier, S.,
Saulin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissensbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)

2 (bases 1 to 869)
Toffano-Nioche, C., Artiguenave, F.,
Duchateau-Nguyen, M., Lemaire, M., Marnette, R., Montrocher, R.,
Robert, C., Termier, M., Wincker, P. and Wesolowski-Louvel, M.
Genomic exploration of the hemiascomycetous yeasts: 11.
Kluyveromyces lactis
FEBS Lett. 487 (1), 66-70 (2000)

3 (bases 1 to 869)
Genoscope.
Direct Submision
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 Evry cedex, FRANCE. (E-mail :
segre@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: *Saccharomyces bayanus* var. *uvatum*, *Saccharomyces exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*,
Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

source

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Db 103 ACGTATATCCAGTGTGTAATATATCTCTCTATGCGCAATAAACCTTGAAGTAAACCCA 162
OY 2329 CGTTTCTCAACTTCCGCAACCGGCGGCGGCGCAGCTGTACGGCGAGAGCTTACGTG 2388
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OY 2389 GGTACAGGTACTACGAGTTTGGCGACAAGAGCTCATTTCCCTTTGGCCACGGCTGT 2448
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Db 463 AAATTTGCTTCAACCTGGGCAAAACGAAACAGTCAAGTTTATCTTGAAGATT 522
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Db 523 CTATTTCTTCTTGATGAAGAGAGTGGTGTGTGAGAGCTGTCAGTACAAAG 582
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